PATENT
Customer No. 22,852
Attorney Docket No. 03260.0047-00

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re Application of:	
John Ernest SIMS	Group Art Unit: 1649
Application No.: 09/612,921	Examiner: CHERNYSHEV, OLGA N.
Filed: July 10, 2000	Confirmation No.: 9162
For: IL-1 Delta DNA and Polypeptides	

Commissioner for Patents
P.O. Box 1450
Alexandria, VA 22313-1450

Sir:

DECLARATION UNDER 37 C.F.R. § 1.131

I, John Ernest Sims, state that I am the named applicant of the above-identified application and am the inventor of the subject matter described and claimed therein. Prior to May 15, 1998, I had completed in this country the invention as described and claimed in the above-identified application as evidenced by the following:

1. I have reviewed pending claims 59-62 and 65-67 of the above-identified Application, a copy of which is attached as Exhibit 1.
2. Exhibit 2, a copy of which is attached, describes embodiments of the nucleic acid molecules claimed in claims 59-62 and 65-67 of Exhibit 1.
3. In particular, on page 1 of Exhibit 2, nucleotides 73-540 are the sequence of human IL-1 delta, which is SEQ ID NO:3 of pending claims 59-62 and 65-67 of the above-identified application.

4. Prior to May 15, 1998, I conceived and reduced to practice in this country at least one embodiment of each of the nucleic acid molecules claimed in claims 59-62 and 65-67 of Exhibit 1, as evidenced by Exhibit 2.

5. Prior to May 15, 1998, I requested that one of the researchers working under me have the Immunex sequencing facility sequence several clones of human cDNAs, which had been isolated under my direction. At that time, I believed that these clones contained full-length human IL-1 delta DNA.

6. On information and belief, the researcher completed a DNA Sequence Request Form prior to May 15, 1998, a copy of which is attached as Exhibit 3, and submitted it to the sequencing facility at Immunex Corporation.

7. On information and belief, the sequencing facility at Immunex Corporation completed sequencing the clones and sent the sequences to a computer file prior to May 15, 1998. A copy of a printout of the DNA sequences in that file is attached as Exhibit 2.

8. Prior to May 15, 1998, I examined a printout of the DNA sequences generated from the clones.

9. Prior to May 15, 1998, I confirmed that the sequences contained a complete human IL-1 delta coding region.

10. On information and belief, a printout of the DNA sequences generated from the clones was viewed by another researcher at Immunex Corporation prior to May 15, 1998.

11. Prior to May 15, 1998, I discussed with another researcher at Immunex Corporation that the printout of the DNA sequences generated from the clones contained the sequence of a complete human IL-1 delta coding region.

12. The sequence on page 1 of Exhibit 2 comprises the nucleic acid sequence of SEQ ID NO:3 of the above-identified application.

13. The sequence on page 1 of Exhibit 2 comprises at least 30 contiguous nucleotides of the nucleic acid sequence of SEQ ID NO:3 of the above-identified application.

14. The sequence on page 1 of Exhibit 2 comprises at least 60 contiguous nucleotides of the nucleic acid sequence of SEQ ID NO:3 of the above-identified application.

15. On information and belief, the sequence on page 1 of Exhibit 2 hybridizes to either strand of a denatured, double-stranded DNA comprising the nucleic acid sequence of SEQ ID NO:3 of the above-identified application, wherein the hybridization conditions include 50% formamide and 6XSSC, at 42°C with washing conditions of 68°C, 0.2XSSC, 0.1% SDS.

16. The sequence on page 1 of Exhibit 2 is at least 95% identical to the nucleic acid sequence of SEQ ID NO:3 of the above-identified application.

17. The sequence on page 1 of Exhibit 2 is at least 98% identical to the nucleic acid sequence of SEQ ID NO:3 of the above-identified application.

18. The sequence on page 1 of Exhibit 2 is at least 99% identical to the nucleic acid sequence of SEQ ID NO:3 of the above-identified application.

I declare further that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further, that the statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code, and that such willful false statements may jeopardize the validity of the application or any patents issuing thereon.

Respectfully submitted,

Date: August 3, 2006

John Ernest Sims

Attachments:

Exhibit 1: Pending claims 59-62 and 65-67 of the above identified Application.

Exhibit 2: Printout of DNA sequences with names and dates redacted.

Exhibit 3: DNA Sequence Request Form with names and dates redacted.

EXHIBIT 1

Pending claims 59-62 and 65-67 of U.S. Application No. 09/612,921:

59. An isolated nucleic acid molecule comprising the nucleic acid sequence of SEQ ID NO:3.

60. An isolated nucleic acid molecule comprising at least 30 contiguous nucleotides of the nucleic acid sequence of SEQ ID NO:3.

61. The nucleic acid molecule of claim 60, wherein said nucleic acid molecule comprises at least 60 contiguous nucleotides of the nucleic acid sequence of SEQ ID NO:3.

62. An isolated nucleic acid molecule that hybridizes to either strand of a denatured, double-stranded DNA comprising the nucleic acid sequence of SEQ ID NO:3, wherein the hybridization conditions include 50% formamide and 6XSSC, at 42°C with washing conditions of 68°C, 0.2XSSC, 0.1% SDS.

65. The nucleic acid molecule of claim 62, wherein said nucleic acid molecule is at least 95% identical to the nucleic acid sequence of SEQ ID NO:3.

66. The nucleic acid molecule of claim 65, wherein said nucleic acid molecule is at least 98% identical to the nucleic acid sequence of SEQ ID NO:3.

67. The nucleic acid molecule of claim 66, wherein said nucleic acid molecule is at least 99% identical to the nucleic acid sequence of SEQ ID NO:3

pT7B3-huIL1dF1-633-1 CONFIRMED
SR6347 .SR6347]pT7B3-huIL1df1-633-1.seq
file
T7,Vec2
pT7B3-huIL1df1-633-1 9:50 AM Check: 6784

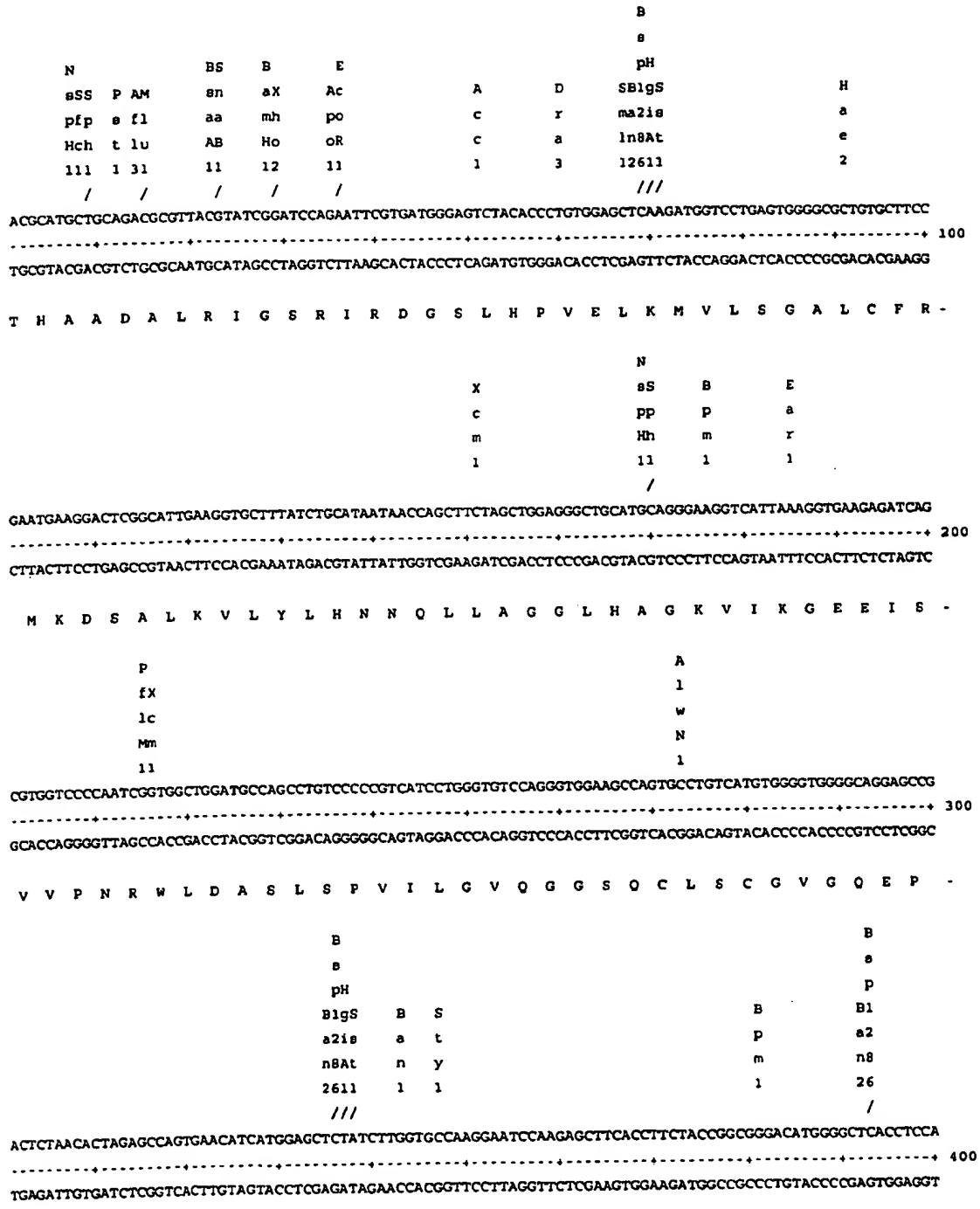
pT7B3-huIL1df1-633-1 Length: 667

```
   1  ACGCATGCTG CAGACGCGTT ACGTATCGGA TCCAGAATTC GTGATGGGAG
  51  TCTACACCCT GTGGAGCTCA AGATGGTCCT GAGTGGGGCG CTGTGCTTCC
 101  GAATGAAGGA CTCGGCATTG AAGGTGCTTT ATCTGCATAA TAACCAGCTT
 151  CTAGCTGGAG GGCTGCATGC AGGGAAGGTC ATTAAAGGTG AAGAGATCAG
 201  CGTGGTCCCC AATCGGTGGC TGGATGCCAG CCTGTCCCCC GTCATCCTGG
 251  GTGTCCAGGG TGGAAGCCAG TGCCTGTCAT GTGGGGTGGG GCAGGAGCCG
 301  ACTCTAACAC TAGAGCCAGT GAACATCATG GAGCTCTATC TTGGTGCCAA
 351  GGAATCCAAG AGCTTCACCT TCTACCGGCG GGACATGGGG CTCACCTCCA
 401  GCTTCGAGTC GGCTGCCTAC CCGGGCTGGT TCCTGTGCAC GGTGCCTGAA
 451  GCCGATCAGC CTGTCAGACT CACCCAGCTT CCCGAGAATG GTGGCTGGAA
 501  TGCCCCCATC ACAGACTTCT ACTTCCAGCA GTGTGACTAG GGCAACGTGC
 551  CCCCCAGAAC TCCCTGGGCA GAGCCAGCTC GGGTGAGGGG TGAGTGGAGG
 601  AGACCCATGG CGGACAATCA CTCATCTGAA TTCGTCGACA AGCTTCTCGA
 651  GCCTAGGCTA GCTCTAG
```

(Linear) (Six Base) MAP of: Pt7b3-Huilldf1-633-1.Seq check: 6784 from: 1 to: 667

pT7B3-huIL1dF1-633-1 CONFIRMED
SR6347
file: .SR6347]pT7B3-huIL1df1-633-1.seq
T7,Vec2
pT7B3-huIL1df1-633-1

With 121 enzymes: *



```
a      T  L  T  L  E  P  V  N  I  M  E  L  Y  L  G  A  K  E  S  K  S  F  T  F  Y  R  R  D  N  G  L  T  S  S -

                                              B
                                              a                               E
                          B             A     pH                              c
          B               AsSX          p     1gB                             o           A
          c               vrmm          a     2ia                             5           v
          g               aFaa          L     8An                             7           a
          1               1111          1     611                             1           1
                          / /                 /
     GCTTCGAGTCGGCTGCCTACCCGGGCTGGTTCCTGTGCACGGTGCCTGAAGCCGATCAGCCTGTCAGACTCACCCAGCTTCCCGAGAATGGTGGCTGGAA
401  ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 500
     CGAAGCTCAGCCGACGGATGGGCCCGACCAAGGACACGTGCCACGGACTTCGGCTAGTCGGACAGTCTGAGTGGGTCGAAGGGCTCTTACCACCGACCTT

a       F  E  S  A  A  Y  P  G  W  F  L  C  T  V  P  E  A  D  Q  P  V  R  L  T  Q  L  P  E  N  G  G  W  N -

                                                          B
                                                          a
                                                          p
        B                                                 1                            A              B
        a                                                 2                            v              a
        m                                                 8                            a              a
        1                                                 6                            1              1
     TGCCCCCATCACAGACTTCTACTTCCAGCAGTGTGACTAGGGCAACGTGCCCCCCAGAACTCCCTGGGCAGAGCCAGCTCGGGTGAGGGGTGAGTGGAGG
501  ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 600
     ACGGGGGTAGTGTCTGAAGATGAAGGTCGTCACACTGATCCCGTTGCACGGGGGGTCTTGAGGGACCCGTCTCGGTCGAGCCCACTCCCCACTCACCTCC

a      A  P  I  T  D  F  Y  F  Q  Q  C  D  *  G  N  V  P  P  R  T  P  W  A  E  P  A  R  V  R  G  E  W  R  -

                                E      H     H
       DNS                      Ac     SAi   i     ASX    AS    N
       act                      po     acn   n     vmh    vt    h
       aoy                      oR     lcc   d     alo    ry    e
       111                      11     112   3     111    21    1
        //                      /                  //     /
     AGACCCATGGCGGACAATCACTCATCTGAATTCGTCGACAAGCTTCTCGAGCCTAGGCTAGCTCTAG
601  ---------+---------+---------+---------+---------+---------+------- 667
     TCTGGGTACCGCCTGTTAGTGAGTAGACTTAAGCAGCTGTTCGAAGAGCTCGGATCCGATCGAGATC

a      R  P  M  A  D  N  H  S  S  E  F  V  D  K  L  L  E  P  R  L  A  L    -
```

Enzymes that do cut:

Acc1	Afl3	AlwN1	Apo1	ApaL1	Ava1	Avr2	BamH1	Ban1	Ban2	Bcg1	Bpm1	Bsa1
BsaA1	Bsm1	Bsp1286	BsrF1	Dra3	Dsa1	Ear1	Eco571	EcoR1	Hae2	HgiA1	Hinc2	Hind3
Mlu1	Nco1	Nhe1	NspH1	PflM1	Pst1	Sal1	Sfc1	Sma1	Sml1	SnaB1	Sph1	Sst1
Sty1	Xcm1	Xho1	Xho2	Xma1								

Enzymes that do not cut:

Aat2	Acl1	Afl2	Age1	Apa1	Asc1	Ase1	Asp718	Asu2	Bal1	Bbs1	BciV1	Bcl1
Bgl1	Bgl2	Bpu1102l	BsaB1	BsaH1	Bsg1	BsiE1	BsiW1	BsmB1	BspE1	BspH1	BspM1	BssH2
BstZ171	BstE2	BstX1	Bsu361	Cla1	Dra1	Dra2	Drd1	Eae1	Eam1105	Eco473	EcoN1	EcoR5
Fse1	Fsp1	Hpa1	Kas1	Kpn1	Mun1	Nar1	Nde1	NgoM1	Not1	Nru1	Nsi1	NspB2
Pac1	Pme1	Pml1	PpuM1	PshA1	Pss1	Pvu1	Pvu2	Rsr2	Sap1	Sca1	Sfi1	SgrA1
Spe1	Srf1	Sse8387	Ssp1	Sst2	Stu1	Swa1	Tth31	Tth32	Xba1	Xma3	Xmn1	

pT7B3-huIL1dF1-633-10 CONFIRMED
SR6347 [redacted] .SR6347]pT7B3-huIL1df1-633-10.seq
file
T7,Vec2
pT7B3-huIL1d-633-10
[redacted] 9:29 AM Check: 2316

pT7B3-huIL1d-633-10 Length: 757

```
   1  CCAGGGTTTT CCCAGTCACG ACGTTGTAAA ACGACGGCCA GTGAATTGTG
  51  CGGCCGCGAG CTCGGGCCCC CACACGTGTG GTCTAGAGCT AGCCTAGGCT
 101  CGAGAAGCTT GTCGACGAAT TCAGATGGGA GTCTACACCC TGTGGAGCTC
 151  AAGATGGTCC TGAGTGGGGC GCTGTGCTTC CGAATGAAGG ACTCGGCATT
 201  GAAGGTGCTT TATCTGCATA ATAACCAGCT TCTAGCTGGA GGGCTGCATG
 251  CAGGGAAGGT CATTAAAGGT GAAGAGATCA GCGTGGTCCC CAATCGGTGG
 301  CTGGATGCCA GCCTGTCCCC CGTCATCCTG GGTGTCCAGG GTGGAAGCCA
 351  GTGCCTGTCA TGTGGGGTGG GGCAGGAGCC GACTCTAACA CTAGAGCCAG
 401  TGAACATCAT GGAGCTCTAT CTTGGTGCCA AGGAATCCAA GAGCTTCACC
 451  TTCTACCGGC GGGACATGGG GCTCACCTCC AGCTTCGAGT CGGCTGCCTA
 501  CCCGGGCTGG TTCCTGTGCA CGGTGCCTGA AGCCGATCAG CCTGTCAGAC
 551  TCACCCAGCT TCCCGAGAAT GGTGGCTGGA ATGCCCCCAT CACAGACTTC
 601  TACTTCCAGC AGTGTGACTA GGGCAACGTG CCCCCCAGAA CTCCCTGGGC
 651  AGAGCCAGCT CGGGTGAGGG GTGAGTGGAG GAGACCCATG GCGGACAATC
 701  ACTCATCACG AATTCTGGAT CCGATACGTA ACGCGTCTGC AGCATGCGTG
 751  GTACCGA
```

(Linear) (Six Base) MAP of: Pt7b3-Huilldfl-633-10.Seq check: 2316 from: 1 to: 757

pT7B3-huIL1dF1-633-10 CONFIRMED
SR6347 [redacted]
file [redacted].SR6347]pT7B3-huIL1df1-633-10.seq
T7,Vec2
pT7B3-huIL1d-633-10

With 121 enzymes: *

10:00 ..

```
                                                                       B      B
                                                                       s      s
                                                              B        pH     p   B B
                                           E              ENXs      AB1gDS AB1PA AsPs     X     N   AS    AS
                                           a              aomi      va2irs pa2sf famt     b     h   vt    vm
                                           e              etaE      an8Aat an8sl 1A1X     a     e   ry    al
                                           1              1131      126121 12613 3111     1     1   21    11
                                                          //        // /   ///    /                  /     /
        CCAGGGTTTTCCCAGTCACGACGTTGTAAAACGACGGCCAGTGAATTGTGCGGCCGCGAGCTCGGGCCCCCACACGTGTGGTCTAGAGCTAGCCTAGGCT
      1 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 100
        GGTCCCAAAAGGGTCAGTGCTGCAACATTTTGCTGCCGGTCACTTAACACGCCGGCGCTCGAGCCCGGGGGTGTGCACACCAGATCTCGATCGGATCCGA

a        P  G  F  S  Q  S  R  R  C  K  T  T  A  S  E  L  C  G  R  E  L  G  P  P  H  V  W  S  R  A  S  L  G  S -

                                                          B
                                                          s
             H       H    E                               pH
        X    i      SAi  Ac             A         D    SB1gS                    H
        h    n      acn  po             c         r    ma2is                    a
        o    d      1cc  oR             c         a    1n8At                    e
        1    3      112  11             1         3    12611                    2
        /                /                              ///
        CGAGAAGCTTGTCGACGAATTCAGATGGGAGTCTACACCCTGTGGAGCTCAAGATGGTCCTGAGTGGGGCGCTGTGCTTCCGAATGAAGGACTCGGCATT
    101 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 200
        GCTCTTCGAACAGCTGCTTAAGTCTACCCTCAGATGTGGGACACCTCGAGTTCTACCAGGACTCACCCCGCGACACGAAGGCTTACTTCCTGAGCCGTAA

a          R  S  L  S  T  N  S  D  G  S  L  H  P  V  E  L  K  M  V  L  S  G  A  L  C  F  R  N  K  D  S  A  L -

                                                          N                                             P
                                       X                 sS     B       E                              fX
                                       c                 pp     p       a                              1c
                                       m                 Hh     m       r                              Mm
                                       1                 11     1       1                              11
                                                         ./
        GAAGGTGCTTTATCTGCATAATAACCAGCTTCTAGCTGGAGGGCTGCATGCAGGGAAGGTCATTAAAGGTGAAGAGATCAGCGTGGTCCCCAATCGGTGG
    201 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 300
        CTTCCACGAAATAGACGTATTATTGGTCGAAGATCGACCTCCCGACGTACGTCCCTTCCAGTAATTTCCACTTCTCTAGTCGCACCAGGGGTTAGCCACC

a         K  V  L  Y  L  H  N  N  Q  L  L  A  G  G  L  H  A  G  K  V  I  K  G  E  E  I  S  V  V  P  N  R  W  -

                                                             A
                                                             l
                                                             w
                                                             N
                                                             1
        CTGGATGCCAGCCTGTCCCCCGTCATCCTGGGTGTCCAGGGTGGAAGCCAGTGCCTGTCATGTGGGGTGGGGCAGGAGCCGACTCTAACACTAGAGCCAG
    301 ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 400
        GACCTACGGTCGGACAGGGGGCAGTAGGACCCACAGGTCCCACCTTCGGTCACGGACAGTACACCCCACCCCGTCCTCGGCTGAGATTGTGATCTCGGTC
```

```
a       L D A S L S P V I L G V Q G G S Q C L S C G V G Q E P T L T L E P V -

                         B                                                        B
                         s                                                        s
                         pH                                                       p
                         BlgS    B   S                                Bl          B1           B
                         a2is    a   t                                p           a2           c
                         n8At    n   y                                m           n8           g
                         2611    1   1                                1           26           1
                         ///                                                      /
        TGAACATCATGGAGCTCTATCTTGGTGCCAAGGAATCCAAGAGCTTCACCTTCTACCGGCGGGACATGGGGCTCACCTCCAGCTTCGAGTCGGCTGCCTA
401     ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 500
        ACTTGTAGTACCTCGAGATAGAACCACGGTTCCTTAGGTTCTCGAAGTGGAAGATGGCCGCCCTGTACCCCGAGTGGAGGTCGAAGCTCAGCCGACGGAT

a         N I M E L Y L G A K E S K S F T F Y R R D M G L T S S F E S A A Y -

                            B
                            s                           E
        B              A    pH                          c
        AsSX           p    lgB                         o            A                      B
        vrmm           a    2ia                         5            v                      s
        aFaa           L    8An                         7            a                      m
        1111           1    611                         1            1                      1
         / /                 /
        CCCGGGCTGGTTCCTGTGCACGGTGCCTGAAGCCGATCAGCCTGTCAGACTCACCCAGCTTCCCGAGAATGGTGGCTGGAATGCCCCCATCACAGACTTC
501     ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 600
        GGGCCCGACCAAGGACACGTGCCACGGACTTCGGCTAGTCGGACAGTCTGAGTGGGTCGAAGGGCTCTTACCACCGACCTTACGGGGGTAGTGTCTGAAG

a       P G W F L C T V P E A D Q P V R L T Q L P E N G G W N A P I T D F -

                                       B
                                       s
                                       p
                                       1                          A               B           DNS
                                       2                          v               s           act
                                       8                          a               a           aoy
                                       6                          1               1           111
                                                                                               //
        TACTTCCAGCAGTGTGACTAGGGCAACGTGCCCCCCAGAACTCCCTGGGCAGAGCCAGCTCGGGTGAGGGGTGAGTGGAGGAGACCCATGGCGGACAATC
601     ---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+ 700
        ATGAAGGTCGTCACACTGATCCCGTTGCACGGGGGGTCTTGAGGGACCCGTCTCGGTCGAGCCCACTCCCCACTCACCTCCTCTGGGTACCGCCTGTTAG

a       Y F Q Q C D * G N V P P R T P W A E P A R V R G E W R R P M A D N H -

                                                          A
                  E     B         BS                  N   s
                  Ac    aX        sn  AM  S   P       sS  pB  K
                  po    mh        aa  fl  f   s       pp  7a  p
                  oR    Ho        AB  lu  c   t       Hh  1n  n
                  11    12        11  31  1   1       11  81  1
                   /     /         /   /               /   /
        ACTCATCACGAATTCTGGATCCGATACGTAACGCGTCTGCAGCATGCGTGGTACCGA
701     ---------+---------+---------+---------+---------+------- 757
        TGAGTAGTGCTTAAGACCTAGGCTATGCATTGCGCAGACGTCGTACGCACCATGGCT

a        S S R I L D P I R N A S A A C V V P  -
```

Enzymes that do cut:

immunex

Priority #2

DNA SEQUENCE REQUEST FORM

RESEARCHER [redacted] X _____ *attach photo here*

CURRENT DATE: _____

PROJECT NAME: GENE DISCOVERY
(to charge time to)

PCR fragments-5ul of sample
w. 200ng PhiX-Hae3
1.5% agarose / TAE gel
ethidium stain after running

NAME OF CLONE(s): pT7B3-hu IL17 f1 # 633-1, 633-8, 633-10 → SR6069, SR6258

Has this been sequenced at Immunex? SEQ REQ#_____ BY _____
VAX file location & name [redacted] IL17D. HIL17HUIL17D-FL.R. SEQ
[directory.subdir]filename (or attach seq)

Has this been sequenced previously and published?
Accession# _____ or Vax file location_____

DNA PREP METHOD: (circle) PEG ppt'd. : YES
DIRT. Maxi=Qiagen-500. PCR. Other:_____
Maxi prep # _____

COMMENTS: (Pertinent Information. amount of sequence needed. available oligos. PCR amplification primers. insert size etc.)

insert ~550 *bases*

vector pT7Blue 3 *cloning site*
cloning site (EcoRI)

full length human IL-17d/17b cloned into pT7Blue 3. Please generate complete ds sequence of ent. I need one that is free of PCR errors. + lots of oligos available if needed

Thanks,
[redacted]

Date started: [redacted] Req#: 6347

Date completed: Sequencer:

✓ sent to sr_database Vax file location: [_____ . SR6347]

Run each # T7 + Vec 2 1/4 BD, 250 ng DNA

pBS

3m 26 25

Made contigs – export to VAX
Did bestfits

Made maps – gave to Blair. Done.

#1 + 11 are correct

#8 has one change. 3 Cont